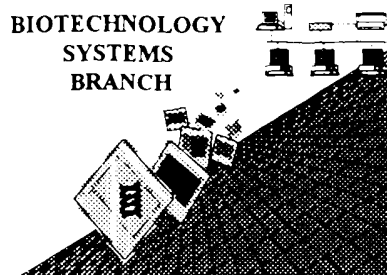**BIOTECHNOLOGY SYSTEMS BRANCH**

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/018,311_

Source: _Pur/10_

Date Processed by STIC: _1/9/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual** - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
       Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/018,311_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAF

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5* amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT10

RAW SEQUENCE LISTING   DATE: 01/09/2002
PATENT APPLICATION: US/10/018,311   TIME: 13:53:13

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01082002\J018311.raw**

```
 5 <110> APPLICANT: MIYATA, Toshio
 7        KUROKAWA, Kiyoshi
11 <120> TITLE OF INVENTION: Meg-3 protein
15 <130> FILE REFERENCE: 2605/101
19 <140> CURRENT APPLICATION NUMBER: US/10/018,311
21 <141> CURRENT FILING DATE: 2001-10-30
25 <160> NUMBER OF SEQ ID NOS: 8
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
953 <210> SEQ ID NO: 8
955 <211> LENGTH: 29
957 <212> TYPE: DNA
959 <213> ORGANISM: Artificial Sequence
963 <220> FEATURE:
965 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
967        Synthesized Primer Sequence
971 <400> SEQUENCE: 8
E--> 973 gcgaattcga actcagtctg cacccctgc
```

*29 ← insert cumulative base
total at right margin
of each line*

see p. 3 for more error

<210> 1

<211> 3768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(2251)

<400> 1

caggaactgg gccagctccg gtcccttcct tttggggctc tcactctgga gg atg ggg 58

                                                          Met Gly

                                                         1

tgg atg gga gaa aaa acc ggg aag atc ctg acg gag ttc ctc cag ttc   106

Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe

        5   10   15

tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag   154

Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu

       20   25   30

att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg cgc aag gtg   202

Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val

 35   40   45   50

cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag   250

Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln

           55   60   65

```
ctggggagcc ggacggggct cctgaggggt acaggttggg tgggccctcc ctgagggtct 3231

ggggtcaggc tttggcctct gctgcctctc agtcaccaag tcacctccct ctgaaaatcc 3291

agtcccttct ttggatgtcc ttgtgagtca ctctgggcct ggctgtcgtc cctcctcagc 3351

ttcttgttcc tgggacaagg gtcaagccag gatgggccca ggcntgggat cccccacccc 3411

aggaccccac aggccccctc ccctgntgnt ttgcgggggg cagggcagaa atggactcct 3471

tttgggtccc cgaggtgggg tcccctccca gccctgcatc ctccgtgccc tagacctgct 3531

ccccagagga ggggccttga cccacaggaa gtgtggtggc gcctggcaat cagggacccc 3591

cagctgccgc agccctggtt tttggcgcat cttttccctc ttgtcccgaa gatttgcgcc 3651

tttagtgcct tttgaggggt tcccatcatc cctccctgat attgtattga aaatattatg 3711

cacactgttc atgctttttac taatcaataa acgctttatt taaaaaaaaa aaaaaaa    3768
```

VERIFICATION SUMMARY   DATE: 01/09/2002
PATENT APPLICATION: US/10/018,311   TIME: 13 53:14

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01082002\J018311.raw**

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number
L:501 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:505 M:258 W. Mandatory Feature missing, <223> not found for SEQ ID#:1
L:505 M:341 W. (46) "n" or "Xaa" used, for SEQ ID#:1
L:973 M:254 E. No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:8